F Harold .

● 1646

> **This Raw Listing contains the General Information Section and up to first 5 pages.**

ENTERED

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 1   <110> APPLICANT: Hyseq, Inc.
 2   <120> TITLE OF INVENTION: A NOVEL EGF MOTIF PROTEIN OBTAINED FROM
 3         A cDNA LIBRARY OF FETAL LIVER-SPLEEN
 4   <130> FILE REFERENCE: 20411-720
 5   <140> CURRENT APPLICATION NUMBER: US/08/968,800
 6   <141> CURRENT FILING DATE: 1997-11-22
 7   <160> NUMBER OF SEQ ID NOS: 20
 8   <170> SOFTWARE: FastSEQ for Windows Version 3.0
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22          1               5                  10                  15
23         gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt      96
24         Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
25                        20                  25                  30
26         cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga     144
27         Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
28                  35                  40                  45
29         atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc     192
30         Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
31              50                  55                  60
32         tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg     240
33         Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
34              65                  70                  75                  80
35         tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt     288
36         Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
37                        85                  90                  95
38         gaa gac aca gaa                                                     300
39         Glu Asp Thr Glu
40                        100
41   <210> SEQ ID NO 2
42   <211> LENGTH: 1611
43   <212> TYPE: DNA
44   <213> ORGANISM: Homo sapiens
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55        gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt        96
56        Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
57                       20                  25                  30
58        cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga       144
59        Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
60                   35                  40                  45
61        atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc       192
62        Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
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65        Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
66             65                  70                  75                  80
67        tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt       288
68        Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
69                       85                  90                  95
70        gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc       336
71        Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
72                   100                 105                 110
73        cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc       384
74        Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
75                   115                 120                 125
76        tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt       432
77        Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
78             130                 135                 140
79        gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc       480
80        Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
81        145                 150                 155                 160
82        agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc       528
83        Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
84                       165                 170                 175
85        cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc       576
86        His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
87                       180                 185                 190
88        aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct       624
89        Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
90                   195                 200                 205
91        gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc       672
92        Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
93                   210                 215                 220
94        atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa       720
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 96        225             230             235             240
 97        aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct    768
 98        Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
 99                        245             250             255
100        acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc    816
101        Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
102                        260             265             270
103        aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg    864
104        Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
105                    275             280             285
106        aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat    912
107        Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
108            290             295             300
109        gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg    960
110        Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
111        305             310             315             320
112        aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta   1008
113        Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
114                        325             330             335
115        act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc   1056
116        Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
117                        340             345             350
118        ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt   1104
119        Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
120                        355             360             365
121        gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca   1152
122        Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
123                370             375             380
124        gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt   1200
125        Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
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127        ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat   1248
128        Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
129                        405             410             415
130        tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa   1296
131        Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
132                    420             425             430
133        aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa   1344
134        Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
135                435             440             445
136        aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc   1392
137        Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
138            450             455             460
139        aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa   1440
140        Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
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142        atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc   1488
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       161          Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
       162                  50                  55                  60
       163          Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
       164          65                  70                  75                  80
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       184          Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
       185                  50                  55                  60
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       187          65                  70                  75                  80
       188          Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
       189                          85                  90                  95
       190          Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
       191                         100                 105                 110
       192          Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
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       194          Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
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197     145                150                155                160
198     Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
199                      165                170                175
200     His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
201                      180                185                190
202     Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
203                      195                200                205
204     Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
205                      210                215                220
206     Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
207     225                230                235                240
208     Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
209                      245                250                255
210     Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
211                      260                265                270
212     Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
213                      275                280                285
214     Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
215                      290                295                300
216     Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
217     305                310                315                320
218     Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
219                      325                330                335
220     Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
221                      340                345                350
222     Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
223                      355                360                365
224     Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
225     370                375                380
226     Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
227     385                390                395                400
228     Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
229                      405                410                415
230     Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
231                      420                425                430
232     Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
233                      435                440                445
234     Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
235     450                455                460
236     Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
237     465                470                475                480
238     Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
239                      485                490                495
240     Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu
241                      500                505                510
242     Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly
243                      515                520                525
244     Ile Leu Lys Leu Leu Ala Glu Lys Leu
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Line	?	Error/Warning	Original Text
35	W	"N" or "Xaa" used: Feature required	tgt gtg aac tcn agg aca tgt gcc atg ata a
67	W	"N" or "Xaa" used: Feature required	tgt gtg aac tcn agg aca tgt gcc atg ata a
145	W	"N" or "Xaa" used: Feature required	ctt tta tct gtg gan nnc tgaatggtac tatctt
240	W	"N" or "Xaa" used: Feature required	Leu Leu Ser Val Asp Asp Xaa Met Val Leu S
255	W	"N" or "Xaa" used: Feature required	Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln A
257	W	"N" or "Xaa" used: Feature required	Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys X
259	W	"N" or "Xaa" used: Feature required	Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
270	W	"N" or "Xaa" used: Feature required	Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys G
272	W	"N" or "Xaa" used: Feature required	Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys C
274	W	"N" or "Xaa" used: Feature required	Gly Xaa Xaa Leu Xaa Cys Asp
311	W	"N" or "Xaa" used: Feature required	Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa X
313	W	"N" or "Xaa" used: Feature required	Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa C
315	W	"N" or "Xaa" used: Feature required	Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa X
330	W	"N" or "Xaa" used: Feature required	Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly G
347	W	"N" or "Xaa" used: Feature required	ccttttntt tttgg
361	W	"N" or "Xaa" used: Feature required	ccaaaaanaa aaagg